

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/089,057A
Source: IFW/6
Date Processed by STIC: 10/18/04

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,057A

DATE: 10/18/2004

TIME: 09:38:04

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10182004\J089057A.raw

3 <110> APPLICANT: HIRANO, SEIKO
 4 KIMURA, EIICHIRO
 5 OSUMI, TSUYOSHI
 6 MATSUI, KAZUHIKO
 7 KAWAHARA, YOSHIO
 8 NONAKA, GEN
 9 MATSUZAKI, YUMI
 10 AKIYOSHI, NAOKI
 11 NAKAMURA, KANAE
 12 KURAHASHI, OSAMU
 13 NAKAMATSU, TSUYOSHI
 14 SUGIMOTO, SHINICHI
 16 <120> TITLE OF INVENTION: GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY
 17 DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA
 W--> 18 <130> FILE REFERENCE: 221519US0PCT
 20 <140> CURRENT APPLICATION NUMBER: 10/089,057A
 21 <141> CURRENT FILING DATE: 2002-04-03
 23 <150> PRIOR APPLICATION NUMBER: PCT/JP00/06913
 24 <151> PRIOR FILING DATE: 2000-10-04
 26 <150> PRIOR APPLICATION NUMBER: JP 11-282716
 27 <151> PRIOR FILING DATE: 1999-10-04
 29 <150> PRIOR APPLICATION NUMBER: JP 11-311147
 30 <151> PRIOR FILING DATE: 1999-11-01
 32 <150> PRIOR APPLICATION NUMBER: JP 2000-120687
 33 <151> PRIOR FILING DATE: 2000-04-21
 35 <160> NUMBER OF SEQ ID NOS: 108
 37 <170> SOFTWARE: PatentIn version 3.1
 39 <210> SEQ ID NO: 1
 40 <211> LENGTH: 1980
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Corynebacterium thermoaminogenes
 44 <220> FEATURE:
 45 <221> NAME/KEY: CDS
 46 <222> LOCATION: (577)..(1869)
 48 <400> SEQUENCE: 1
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 50 atgcaaagct cttcgaaagc aagagatcg gtgtgtcg ggacccatcg gggaaagccc 120
 51 tcgctgcgcc ccagggggag ctggcgatgt gaccaggta agtataacc atcaccttgc 180
 52 caatgggtt gcaacttta ccgtgacgct acccccgctt ttgtttgatc acaccagctc 240
 53 gaaggctgtc gctttccga agatgcacgt gaagtggcaa atccttgcca cccgaggttt 300
 54 tcccaagtaca aacgtactag tgatgaggat cacggggAAC attgtggaga ttgcactttg 360
 55 caatatttgc aaaagggtg actaccccccg cgcaaaaactt aaaaacccaa atccgttgac 420
 56 ggaccatgc ccgatgaagc aatgtgtgaa gcacgcccacc ggaacacagg ttgtggatca 480

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57	ctcaccatga	tgtggggat	tcgcatacaca	cagtgtgcag	ggccggcacct	ctaccgaatg	540										
58	cgccttacag	cagcaccaag	aagaagtgac	tcttag	atg	tca	aac	gtt	gga	acg	594						
59							Met	Ser	Asn	Val	Gly	Thr					
60							1					5					
61	cca	cgt	acc	gca	cag	gaa	atc	cag	cag	gat	tgg	gac	acc	aac	cca	cgc	642
62	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro	Arg	
63							10				15			20			
64	tgg	aat	gga	atc	acc	cgc	gac	tac	acc	gct	gag	cag	gta	gct	gag	ctc	690
65	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Glu	Gln	Val	Ala	Glu	Leu	
66							25				30			35			
67	cag	ggc	agc	gtc	gtc	gag	gag	cac	acc	ctc	gca	aag	cgc	ggc	gcc	gag	738
68	Gln	Gly	Ser	Val	Val	Glu	Glu	His	Thr	Leu	Ala	Lys	Arg	Gly	Ala	Glu	
69							40				45			50			
70	atc	ctg	tgg	aat	gca	gtt	tcc	gca	gag	ggc	gac	gac	tac	atc	aac	gca	786
71	Ile	Leu	Trp	Asp	Ala	Val	Ser	Ala	Glu	Gly	Asp	Asp	Tyr	Ile	Asn	Ala	
72							55				60			65			70
73	ctg	ggc	gcc	ctt	acc	ggt	aat	cag	gct	gtc	cag	cag	gtc	cgt	gcc	ggc	834
74	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val	Gln	Gln	Val	Arg	Ala	Gly	
75							75				80			85			
76	ctg	aag	gct	gtc	tac	tcc	ggc	tgg	cag	gtc	gca	ggt	gac	gcc	aac	882	
77	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala	Asn	
78							90				95			100			
79	ctc	gcc	ggt	cac	acc	tac	ccc	gac	cag	tcc	ctg	tac	ccg	gcg	aac	tcc	930
80	Leu	Ala	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn	Ser	
81							105				110			115			
82	gtc	ccg	aac	gtt	gtc	cgt	cgc	atc	aac	aac	gca	ctg	ctg	cgc	gcc	gat	978
83	Val	Pro	Asn	Val	Val	Arg	Arg	Ile	Asn	Asn	Ala	Leu	Leu	Arg	Ala	Asp	
84							120				125			130			
85	gag	atc	gca	cgc	gtc	gag	ggt	gac	acc	tcc	gtc	gac	aac	tgg	ctc	gtc	1026
86	Glu	Ile	Ala	Arg	Val	Glu	Gly	Asp	Thr	Ser	Val	Asp	Asn	Trp	Leu	Val	
87							135				140			145			150
88	ccg	atc	gtc	gcc	gac	ggc	gag	gcc	ggc	tcc	ggt	ggc	gcc	ctc	aac	gtc	1074
89	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe	Gly	Gly	Ala	Leu	Asn	Val	
90							155				160			165			
91	tac	gag	ctc	cag	aag	ggc	atg	atc	acc	gct	ggt	gcc	gca	ggc	acc	cac	1122
92	Tyr	Glu	Leu	Gln	Lys	Gly	Met	Ile	Thr	Ala	Gly	Ala	Ala	Gly	Thr	His	
93							170				175			180			
94	tgg	gag	aat	gtc	ctc	gct	tcc	gag	aag	aag	tgt	ggc	cac	ctc	ggt	ggc	1170
95	Trp	Glu	Asp	Gln	Leu	Ala	Ser	Glu	Lys	Lys	Cys	Gly	His	Leu	Gly	Gly	
96							185				190			195			
97	aag	gtc	ctc	atc	ccg	acc	cag	cag	cac	atc	cgc	acc	ctg	aac	tcc	gcc	1218
98	Lys	Val	Leu	Ile	Pro	Thr	Gln	Gln	His	Ile	Arg	Thr	Leu	Asn	Ser	Ala	
99							200				205			210			
100	cgc	ctg	gca	gct	gac	gtg	gcc	aac	acc	ccg	acc	gtc	atc	gcc	cgc		1266
101	Arg	Leu	Ala	Ala	Asp	Val	Ala	Asn	Thr	Pro	Thr	Val	Val	Ile	Ala	Arg	
102							215				220			225			230
103	acc	gac	gca	gag	gcc	gcc	acc	ctg	atc	acc	tct	gat	gtt	gat	gag	cgc	1314
104	Thr	Asp	Ala	Glu	Ala	Ala	Thr	Leu	Ile	Thr	Ser	Asp	Val	Asp	Glu	Arg	
105							235				240			245			

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106 gac cgc cca ttc atc acc ggc gag cgc acc gcc gag ggc tac tac cac 1362
 107 Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr His
 108 250 255 260
 109 gtc aag ccg ggt ctc gag ccc tgc atc gca cgt gcg aag tcc tac gct 1410
 110 Val Lys Pro Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr Ala
 111 265 270 275
 112 ccc tac gca gac atg atc tgg atg gag acc ggc acc cct gac ctc gag 1458
 113 Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu Glu
 114 280 285 290
 115 ctg gcc aag aag ttc gcc gag ggc gtc cgc agc gag ttc ccg gac cag 1506
 116 Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp Gln
 117 295 300 305 310
 118 ctg ctg tcc tac aac tgc tcc ccg tcc ttc aac tgg tct gca cac ctc 1554
 119 Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His Leu
 120 315 320 325
 121 gag gcc gac gag atc gct aag ttc cag aag gaa ctg ggt gcc atg ggc 1602
 122 Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met Gly
 123 330 335 340
 124 ttc aag ttc cag ttc atc acc ctg gct ggc ttc cac tcc ctc aac tac 1650
 125 Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn Tyr
 126 345 350 355
 127 ggt atg ttc gac ctg gct tac ggc tac gcc cgt gaa ggc atg ccc gcc 1698
 128 Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Pro Ala
 129 360 365 370
 130 ttc gtc gac ctg cag aac cgt gag ttc aag gca gct gag gag cgc ggc 1746
 131 Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg Gly
 132 375 380 385 390
 133 ttc acc gcc gtc aag cac cag cgt gag gtc ggc ggc tac ttc gac 1794
 134 Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe Asp
 135 395 400 405
 136 acc atc gcc acc acc gtt gac ccg aac tcc tcc acc acc gcg ctg aag 1842
 137 Thr Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu Lys
 138 410 415 420
 139 ggt tcc acc gag gaa tgc cag ttc cac taggaaccac ctgatgcgg 1889
 140 Gly Ser Thr Glu Glu Cys Gln Phe His
 141 425 430
 142 gccgtatggc ctgacggcac cgccccctccc tttgcactcc agtactcctt tgtgcacatc 1949
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 145 <210> SEQ ID NO: 2
 146 <211> LENGTH: 431
 147 <212> TYPE: PRT
 148 <213> ORGANISM: Corynebacterium thermoaminogenes
 150 <400> SEQUENCE: 2
 151 Met Ser Asn Val Gly Thr Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
 152 1 5 10 15
 153 Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
 154 20 25 30
 155 Glu Gln Val Ala Glu Leu Gln Gly Ser Val Val Glu Glu His Thr Leu
 156 35 40 45

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157 Ala Lys Arg Gly Ala Glu Ile Leu Trp Asp Ala Val Ser Ala Glu Gly
 158 50 55 60
 159 Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 160 65 70 75 80
 161 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 162 85 90 95
 163 Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
 164 100 105 110
 165 Leu Tyr Pro Ala Asn Ser Val Pro Asn Val Val Arg Arg Ile Asn Asn
 166 115 120 125
 167 Ala Leu Leu Arg Ala Asp Glu Ile Ala Arg Val Glu Gly Asp Thr Ser
 168 130 135 140
 169 Val Asp Asn Trp Leu Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 170 145 150 155 160
 171 Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala
 172 165 170 175
 173 Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 174 180 185 190
 175 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 176 195 200 205
 177 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 178 210 215 220
 179 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 180 225 230 235 240
 181 Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr
 182 245 250 255
 183 Ala Glu Gly Tyr Tyr His Val Lys Pro Gly Leu Glu Pro Cys Ile Ala
 184 260 265 270
 185 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 186 275 280 285
 187 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 188 290 295 300
 189 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 190 305 310 315 320
 191 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 192 325 330 335
 193 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 194 340 345 350
 195 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 196 355 360 365
 197 Arg Glu Gly Met Pro Ala Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 198 370 375 380
 199 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
 200 385 390 395 400
 201 Gly Ala Gly Tyr Phe Asp Thr Ile Ala Thr Thr Val Asp Pro Asn Ser
 202 405 410 415
 203 Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Cys Gln Phe His
 204 420 425 430
 206 <210> SEQ ID NO: 3

RAW SEQUENCE LISTING DATE: 10/18/2004
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Input Set : A:\PTO.FG.txt
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207 <211> LENGTH: 2381
208 <212> TYPE: DNA
209 <213> ORGANISM: Corynebacterium thermoaminogenes
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (577)..(2349)
215 <400> SEQUENCE: 3
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218 acacctgggt cgtgttgaag tacctgtgg gtttgaaaaa cgtccgcaac tatgacggtt 180
219 cctggtcga gtggggcaac atggtgcgca tgcccatcgt ccagggtgat gagccggct 240
220 cactctagtc accccggggt cacctccctg gtcacccccc taccctcccc ggtacacccc 300
221 ggggacgggg tgtgacctgg atctccctg catgtggaca cgggaaact ttgcctggaa 360
222 aatgaccatc cagtaccgta atgcgggtat gtaacgcgg tcacaggta caccagaatc 420
223 cggatcgct aacccctta gcgggattcg ctaaaagatc accgagttag tgtgcaagaa 480
224 taatgctgat cgcaggggca ctgtcatacg ctgtcatgca gtcaatgaac agtgcgggtgc 540
225 tctgtcgtga agaaaatcaa aaccaggagg gttta gtg tca gtc gag acc agg 594
226 Val Ser Val Glu Thr Arg
227 1 5
228 aag atc acc aag gta ctt gtc gcc aac cgt ggt gaa atc gca atc cgt 642
229 Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile Arg
230 10 15 20
231 gtt ttc cgc gca gca cgg gat gaa ggc atc gcc tct gtc gcc gtc tac 690
232 Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr
233 25 30 35
234 gcg gag ccg gac gca gat gcc cct ttc gtc gag tat gcc gat gag gcc 738
235 Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Glu Tyr Ala Asp Glu Ala
236 40 45 50
237 ttc gca ctc ggt ggc cag act tcc gca gag tcc tac ctc gtc att gac 786
238 Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp
239 55 60 65 70
240 aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc 834
241 Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pro
242 75 80 85
243 ggc tac ggc ttc ctc gcc gag aac gcc gat ttc gct gaa gct gtc atc 882
244 Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
245 90 95 100
246 aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc 930
247 Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
248 105 110 115
249 ctc ggt gac aag gtc acc gca cgc cac atc gcc aac aac gcc aac gca 978
250 Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
251 120 125 130
252 ccg atg gca ccg ggc acc aag gag cct gtc aag gac gcc gct gag gtt 1026
253 Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu Val
254 135 140 145 150
255 gtc gcc ttc gcc gag gag ttc ggt ctc ccc atc gcc atc aag gct gcc 1074
256 Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala Ala
257 155 160 165

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 3
Seq#:46; N Pos. 18
Seq#:55; N Pos. 3,6,9
Seq#:56; N Pos. 3,9,18
Seq#:83; N Pos. 9

VERIFICATION SUMMARY

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:18 M:283 W: Missing Blank Line separator, <130> field identifier
3855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
3871 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
3985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
4011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
4606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0